

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 9, 2002, 20:03:52 ; Search time 11.88 seconds

(Without alignments)
338.959 Million cell updates/sec

Title: US-09-622-613a-2

Perfect score: 576

Sequence: 1 ODWLTFQKKHLNTRDYDCN.....TFCVTCENQAPVHEVGSHC 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	ID	Description
1	547	95.0	104	1	RN30_RANPI
2	291	50.5	111	1	RNPO_RANCA
3	284.5	49.4	111	1	LECS_RANJA
4	268.5	46.6	111	1	RNPL_RANCA
5	154	26.7	119	1	RNP_IGUG
6	130.5	22.7	145	1	RNP_MOUSE
7	128	22.2	124	1	RNP_GALMU
8	125	21.7	128	1	RNPB_CAVPO
9	124	21.5	125	1	RNPI_BOVIN
10	123	21.4	128	1	RNP_MYOCO
11	122	21.2	124	1	RNP_BALAC
12	121	21.0	128	1	RNP_PROGU
13	118.5	20.6	145	1	RNP_MOUSE
14	117	20.3	145	1	RNP_MOUSE
15	116.5	20.2	147	1	RNLA_HUMAN
16	116	20.1	125	1	RNPI_BOVIN
17	114	19.8	124	1	RNPI_BOVIN
18	114	19.8	124	1	RNPI_BOVIN
19	113.5	19.7	125	1	RNPI_BOVIN
20	113	19.6	128	1	RNPI_BOVIN
21	112	19.4	147	1	RNPI_BOVIN
22	112	19.4	147	1	RNPI_BOVIN
23	111	19.3	124	1	RNPI_BOVIN
24	111	19.3	124	1	RNPI_BOVIN
25	109.5	19.0	123	1	RNPI_BOVIN
26	109	18.9	150	1	RNPI_BOVIN
27	109	18.9	156	1	RNPI_BOVIN
28	108	18.8	123	1	RNPI_BOVIN
29	108	18.8	128	1	RNPI_BOVIN
30	108	18.8	128	1	RNPI_BOVIN
31	108	18.8	167	1	RNPI_BOVIN
32	107	18.6	141	1	RNPI_BOVIN
33	107	18.6	151	1	RNPI_BOVIN

ALIGNMENTS

RESULT ID	1	STANDARD:	PRT:	104 AA.
AC	P22069:			
DT	01-AUG-1991 (rel. 19, Created)			
DT	01-FEB-1994 (rel. 28, Last sequence update)			
DT	01-FEB-1995 (rel. 31, Last annotation update)			
DE	P-30 protein (EC 3.1.27.-) (Concanase).			
OS	Rana pipiens (Northern leopard frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.			
OX	NCBI_TaxID=8404;			
RN	[1]			
RP	SEQUENCE.			
RC	TISSUE=Embryo;			
RX	MEDLINE=91093131; PubMed=1985896;			
RA	Ardelt W., Mikulski S.M., Shogen K.;			
RT	"Amino acid sequence of an anti-tumor protein from Rana pipiens oocytes and early embryos. Homology to pancreatic ribonucleases.";			
RL	J. Biol. Chem. 266:245-251(1991).			
RN	[2]			
RP	3D-STRUCTURE MODELING.			
RX	MEDLINE=93066156; PubMed=1438177;			
RA	Mostmann S.C., Johns K.L., Ardelt W., Mikulski S.M., Shogen K., James M.N.G.;			
RT	"Comparative molecular modeling and crystallization of P-30 protein: a novel antitumor protein of Rana pipiens oocytes and early embryos.";			
RL	Proteins 14:392-400(1992).			
RN	[3]			
RP	X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).			
RX	MEDLINE=94166079; PubMed=8120892;			
RA	Mostmann S.C., Ardelt W., James M.N.G.;			
RT	"Refined 1.7 A X-ray crystallographic structure of P-30 protein, an amphibian ribonuclease with anti-tumor activity.";			
RL	J. Mol. Biol. 236:1141-1153(1994).			
CC	- FUNCTION: BASIC PROTEIN WITH ANTIPROLIFERATIVE/CYTOTOXIC ACTIVITY AGAINST SEVERAL TUMOR CELL LINES IN VITRO, AS WELL AS ANTITUMOR IN VIVO. IT EXHIBITS A RIBONUCLEASE-LIKE ACTIVITY AGAINST HIGH MOLECULAR WEIGHT RIBOSOMAL RNA.			
CC	- DEVELOPMENTAL STAGE: EARLY EMBRYOS (UP TO FOUR BLASTOMERE STAGE).			
CC	- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.			
DR	PDB: 1ONC; 31-JAN-94.			
DR	InterPro: IPR001427; RNaseA.			
DR	Pfam: PF00074; rnaasea.1.			
DR	Prodom: PD000535; RNaseA.1.			
DR	SMART: SM00092; RNaseA_Pc.1.			
DR	PROSITE: PS00127; RNASE_PANCREATIC.1.			
KW	Hydrolase; Nuclease; Endonuclease; 3D-structure.			
FT	MOD_RES			
FT	ACT_SITE			
FT	ACT_SITE			
FT	ACT_SITE			
FT	DISULFID			
FT	DISULFID			
FT	DISULFID			



```

FT DISULFID 87 104
FT HELIX 3 10
FT STRAND 11 12
FT HELIX 19 22
FT TURN 23 24
FT TURN 26 30
FT STRAND 33 38
FT HELIX 41 48
FT TURN 49 50
FT STRAND 55 58
FT STRAND 63 70
FT TURN 74 75
FT STRAND 77 84
FT STRAND 86 91
FT TURN 92 93
FT STRAND 101 101
SQ SEQUENCE 104 AA; 11845 MW; 22A753C2F9E566B4 CRC64;

Query Match
Best Local Similarity 95.0%; Score 547; DB 1; Length 104;
Matches 99; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 QDMTFQKKHLNTRDVCNINMTLFFHCKDKNFTFSRPEPVKAICGIIASKNVLT 60
DB 1 QDMTFQKKHLNTRDVCNINMTLFFHCKDKNFTFSRPEPVKAICGIIASKNVLT 60
OY 61 SEFYLSDCNVTSPCKYKLLKSTNTEFCVTCENQAPVHFVGHC 104
DB 61 SEFYLSDCNVTSPCKYKLLKSTNTEFCVTCENQAPVHFVGHC 104

RESULT 2
RPMO_RANCA STANDARD; PRT; 111 AA.
ID RNPO_RANCA
AC P1916:
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ribonuclease, oocytes (EC 3.1.27.-) (RC-RNase) (Stallc acid-binding
DE lectin) (SBL-C).
OS Rana catesbeiana (Bull. frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
RP SEQUENCE.
RC TISSUE=Egg;
RX MEDLINE=8729649; PubMed=3304421;
RA Titani K., Takio K., Kuwada M., Nitta K., Sakakibara F., Kawauchi H.,
RA Takayanagi G., Hakomori S.;
RT "Amino acid sequence of stallc acid binding lectin from frog (Rana
RT catesbeiana) eggs."
RL Biochemistry 26:2189-2194(1987).
RN [2]
RP CHARACTERIZATION, AND SEQUENCE OF 59-79.
RX MEDLINE=92220613; PubMed=1373237;
RA Liao Y.-D.;
RT "A pyrimidine-guanine sequence-specific ribonuclease from Rana
RT catesbeiana (bullfrog) oocytes."
RL Nucleic Acids Res. 20:1371-1377(1992).
RN [3]
RP CHARACTERIZATION.
RC TISSUE=Egg;
RX MEDLINE=93192604; PubMed=8448385;
RA Nitta K., Oyama F., Oyama R., Sekiuchi K., Kawauchi H.,
RA Takayanagi Y., Hakomori S., Titani K.;
RT "Ribonuclease activity of stallc acid-binding lectin from Rana
RT catesbeiana eggs."
RL Glycobiology 3:37-45(1993).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=96437383; PubMed=9761686;

```

```

RA Chang C.-F., Chen C., Chen Y.-C., Hom K., Huang R.-F., Huang T.H.;
RT "The solution structure of a cytotoxic ribonuclease from the oocytes
RT of Rana catesbeiana (bullfrog)."
RL J. Mol. Biol. 283:231-244(1998).
CC -1- FUNCTION: PREFERENTIALLY CLEAVES SINGLE-STRANDED RNA AT PYRIMIDINE
CC RESIDUES WITH A 3'-FLANKING GUANINE. HYDROLYSES POLY(U) AND POLY(C)
CC AS SUBSTRATES, AND PREFERENCES THE FORMER.
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO. THIS LECTIN
CC AGGLUTINATES VARIOUS ANIMAL CELLS, INCLUDING NORMAL LYMPHOCYTES,
CC ERYTHROCYTES, AND FIBROBLASTS OF ANIMAL AND HUMAN ORIGIN.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR; A27121; A27121.
DR PDB; 1BC4; 28-OCT-98.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNaseA; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Stallc acid; Lectin; 3D-structure.
FT MOD_RES 1
FT ACT_SITE 10 10
FT ACT_SITE 35 35
FT ACT_SITE 103 103
FT ACT_SITE 19 71
FT DISULFID 34 81
FT DISULFID 52 96
FT DISULFID 93 110
SQ SEQUENCE 111 AA; 12464 MW; 0BC9E5F5729ECF4 CRC64;

```

```

Query Match
Best Local Similarity 49.5%; Score 291; DB 1; Length 111;
Matches 55; Conservative 16; Mismatches 32; Indels 8; Gaps 3;

OY 1 QDMTFQKKHLNTRDVCNINMTLFF---HCKDKNFTFSRPEPVKAICGIIASKN 56
DB 1 QDMTFQKKHLNTRDVCNINMTLFF---HCKDKNFTFSRPEPVKAICGIIASKN 56
OY 57 VLTSEFYLSDCNVTSPCKYKLLKSTNTEFCVTCENQAPVHFVGHC 104
DB 60 VLTSEFYLSDCNVTSPCKYKLLKSTNTEFCVTCENQAPVHFVGHC 104

RESULT 3
LECS_RANJA STANDARD; PRT; 111 AA.
ID LECs_RANJA
AC P18839:
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Stallc acid-binding lectin (EC 3.1.27.-).
OS Rana japonica (Japanese reddish frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8402;
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RC TISSUE=Egg;
RX MEDLINE=91035319; PubMed=2229005;
RA Kamuya Y., Oyama F., Oyama R., Sakakibara F., Nitta K., Kawauchi H.,
RA Takayanagi Y., Titani K.;
RT "Amino acid sequence of a lectin from Japanese frog (Rana japonica)
RT eggs."
RL J. Biochem. 108:139-143(1990).
CC -1- FUNCTION: THE S-LECTINS IN FROG EGGS MAY BE INVOLVED IN THE
CC FERTILIZATION AND DEVELOPMENT OF THE FROG EMBRYO.
CC -1- FUNCTION: THIS LECTIN PREFERENTIALLY AGGLUTINATE A LARGE VARIETY
CC OF TUMOR CELLS, BUT IT DOES NOT AGGLUTINATE NON-TRANSFORMED CELLS
CC AND ERYTHROCYTES.
CC -1- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 3'-PHOSPHOMONO-
CC NUCLEOTIDES AND 3'-PHOSPHOOLIGONUCLEOTIDES ENDING IN C-P OR U-P

```

WITH 2',3'-CYCLIC PHOSPHATE INTERMEDIATES.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0120: JX0120.
 DR HSP: P11916: 1BC4.
 DR InterPro: IPR001427: RNaseA.
 DR Pfam: PF00074: RNaseA; 1.
 DR ProDom: PD000535: RNaseA; 1.
 DR SMART: SM00092: RNase_Pc; 1.
 DR PROSITE: PS00127: RNase_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease; Sialic acid; Lectin.
 FT MOD_RES 1 1
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 103 103
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97
 FT DISULFID 94 111
 SQ SEQUENCE 111 AA; 12326 MW; FDEBDF3834ED679 CRC64;

Query Match 49.4%; Score 284.5; DB 1; Length 111;
 Best Local Similarity 45.0%; Pred. No. 3.6e-24;
 Matches 50; Conservative 19; Mismatches 35; Indels 7; Gaps 2;

OY 1 QDWLTFQKHLLTNRDVCNIIIMSTNLF---HCKDKNTFTYSRPEPYKAIKGIISK 56
 DB 1 QWAKFQKHLLTNRDVCNIIIMSTNLF---HCKDKNTFTYSRPEPYKAIKGIISK 60
 OY 57 VLTSEFYLSDC---NVTSPCKYKLLKSTNTEFCVTCENAPYHVGVC 104
 DB 61 VLTSEFYLSDC---NVTSPCKYKLLKSTNTEFCVTCENAPYHVGVC 111

RESULT 4
 ID RNP_LIGUTG STANDARD; PRT; 111 AA.
 AC P80287;
 DT 01-FEB-1994 (Rel. 14, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Ribonuclease, liver (EC 3.1.27.5).
 OS Rana catesbeiana (Bull frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 OX NCBI_TaxID=8400;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=90130374; PubMed=2613682;
 RA Nitta R., Katayama N., Okabe Y., Iwama M., Watanabe H., Abe Y.,
 RA Okazaki T., Ohgi K., Irie M.;
 RT "Primary structure of a ribonuclease from bullfrog (*Rana catesbeiana*)
 RT liver.";
 RL J. Biochem. 106:729-735(1989).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-
 CC phosphomononucleotides and 3'-phosphooligonucleotides ending in C-
 CC P or U-P with 2',3'-cyclic phosphate intermediates.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR PIR: JX0085: JX0085.
 DR HSP: P11916: 1BC4.
 DR InterPro: IPR001427: RNaseA.
 DR Pfam: PF00074: RNaseA; 1.
 DR ProDom: PD000535: RNaseA; 1.
 DR SMART: SM00092: RNase_Pc; 1.
 DR PROSITE: PS00127: RNase_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease.
 FT MOD_RES 1 1
 FT ACT_SITE 10 10
 FT ACT_SITE 35 35
 FT ACT_SITE 104 104
 FT DISULFID 19 72
 FT DISULFID 34 82
 FT DISULFID 52 97
 FT DISULFID 94 111
 SQ SEQUENCE 111 AA; 12326 MW; FDEBDF3834ED679 CRC64;

FT DISULFID 34 82 BY SIMILARITY.
 FT DISULFID 52 97 BY SIMILARITY.
 FT DISULFID 94 111 PROBABLE
 SQ SEQUENCE 111 AA; 12461 MW; D64BA72456C10788 CRC64;

Query Match 46.6%; Score 268.5; DB 1; Length 111;
 Best Local Similarity 43.2%; Pred. No. 2e-22;
 Matches 48; Conservative 19; Mismatches 37; Indels 7; Gaps 2;

OY 1 QDWLTFQKHLLTNRDVCNIIIMSTNLF---HCKDKNTFTYSRPEPYKAIKGIISK 56
 DB 1 QWAKFQKHLLTNRDVCNIIIMSTNLF---HCKDKNTFTYSRPEPYKAIKGIISK 60
 OY 57 VLTSEFYLSDC---NVTSPCKYKLLKSTNTEFCVTCENAPYHVGVC 104
 DB 61 VLTSEFYLSDC---NVTSPCKYKLLKSTNTEFCVTCENAPYHVGVC 111

RESULT 5
 ID RNP_LIGUTG STANDARD; PRT; 119 AA.
 AC P80287;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DE 01-FEB-1994 (Rel. 28, Last annotation update)
 DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
 OS Iguana iguana (Common Iguana).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Iguania; Iguanidae; Iguaninae; Iguana.
 OX NCBI_TaxID=8517;
 RN (1)
 RP SEQUENCE.
 RC TISSUE=Pancreas;
 RX MEDLINE=9413745; PubMed=8307028;
 RA Zhao W., Beintema J.J., Hofsteenge J.;
 RT "The amino acid sequence of Iguana (*Iguana iguana*) pancreatic
 RT ribonuclease.";
 RL Eur. J. Biochem. 219:641-646(1994).
 CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-
 CC phosphomononucleotides and 3'-phosphooligonucleotides ending in C-
 CC P or U-P with 2',3'-cyclic phosphate intermediates.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: PANCREAS.
 CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
 DR HSP: P00656: 1LSQ.
 DR InterPro: IPR001427: RNaseA.
 DR Pfam: PF00074: RNaseA; 1.
 DR PRINTS: PR00794: RIBONUCLEASE.
 DR ProDom: PD000535: RNaseA; 1.
 DR SMART: SM00092: RNase_Pc; 1.
 DR PROSITE: PS00127: RNase_PANCREATIC; 1.
 KW Hydrolyase; Nuclease; Endonuclease.
 FT MOD_RES 1 1
 FT DISULFID 25 80
 FT DISULFID 35 91
 FT DISULFID 57 106
 FT DISULFID 10 10
 FT ACT_SITE 40 40
 FT ACT_SITE 113 113
 SQ SEQUENCE 119 AA; 13324 MW; 6072FB5B7B15BD5A CRC64;

Query Match 26.7%; Score 154; DB 1; Length 119;
 Best Local Similarity 30.7%; Pred. No. 5.4e-10;
 Matches 35; Conservative 20; Mismatches 43; Indels 16; Gaps 5;

OY 1 QDWLTFQKHLLTNRDVCNIIIMSTNLFCKDKNTFTYSRPEPYKAIKGIISK-K 49
 DB 1 QWAKFQKHLLTNRDVCNIIIMSTNLFCKDKNTFTYSRPEPYKAIKGIISK-K 60
 OY 50 GIASKNVLTSE-FYLSDC---NVTSPCKYKLLKSTNTEFCVTCENAPYHVF 98
 DB 1 GIASKNVLTSE-FYLSDC---NVTSPCKYKLLKSTNTEFCVTCENAPYHVF 111

Db 61 GTHEDNLYDSNESFDTLDCKNVGGTAPDSCKYNGTGTGTRIRIACENNQPVHF 114

RESULT 6

ANGR_MOUSE STANDARD: PRT: 145 AA.

AC Q6438;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Angiogenin-related protein precursor.

GN ANGRP.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RL [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129; TISSUE=Liver;

RX MEDLINE=96079109; PubMed=8530072;

RA Brown W.E., Noble V., Subramanian V., Shapiro R.;

RT "The mouse angiogenin gene family: structures of an angiogenin-related protein gene and two pseudogenes.";

RT Genomics 29:200-206(1995).

RL [1]

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

CC

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@sib-sib.ch).

CC

DR EMBL: U02519; AAA91367.1; -

DR HSP; P03950; 1AAV.

DR MGD; MGI:104984; AngRP.

DR InterPro: IPR001427; RnaseA.

DR Pfam: PF00074; RnaseA; 1.

DR PRINTS: PD00794; RIBONUCLEASE.

DR PRODOM: PD000535; RnaseA; 1.

DR SMART: SMO0092; Rnase_Pc; 1.

DR PROSITE: PS00127; Rnase_PANCREATIC; 1.

KW Signal; Hydrolase; Nuclease; Endonuclease.

FT SIGNAL 1 24

FT CHAIN 25 145

FT MOD_RES 25 25

FT ACT_SITE 37 37

FT ACT_SITE 64 64

FT ACT_SITE 137 137

FT DISULFID 50 104

FT DISULFID 63 115

FT DISULFID 81 130

FT SEQUENCE 145 AA: 16612 MW: 2946EB814429C4AD CRC64;

Query Match 22.7%; Score 130.5; DB 1; Length 145;

Best Local Similarity 38.2%; Pred. No. 2.3e-07;

Matches 29; Conservative 11; Mismatches 29; Indels 7; Gaps 3;

QY 30 CKDKKTFYSRPEVKAIC--KGIASKNV-LTSEFVSLDCNVTSR---PCKYKLKKS 82

DB 63 CKDVTFTFHDFTKNNIKALCGKSGPYGRRLRISKRSFQVYCTCTHKGSRSPRCRYRASKG 122

QY 83 TITPCVTCENQAPVHF 98

DB 123 FRYIIIGENGWPHF 138

RESULT 7

RNP_GALMU STANDARD: PRT: 124 AA.

ID RNP_GALMU

AC P00680;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Ribonuclease pancreatic (EC 3.1.27.5) (Rnase 1) (Rnase A).

GN RNASE1 OR RNS1.

OS Galea musteloides (Culis).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavillidae; Galea.

OX NCBI_Taxid=10146;

RL [1]

RP SEQUENCE.

RC MEDLINE=87036770; PubMed=6571219;

RA Beintema J.J., Neuteboom B.;

RT "Origin of the duplicated ribonuclease gene in guinea-pig: comparison of the amino acid sequences with those of two close relatives: capybara and culis ribonuclease.";

RT J. Mol. Evol. 19:145-152(1983).

RL [1]

CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-phosphomononucleotides and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: PANCREAS.

CC

CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

CC

DR PIR; A00827; NRUI.

DR HSP; P00656; ISRN.

DR InterPro: IPR001427; RnaseA.

DR Pfam: PF00074; RnaseA; 1.

DR PRINTS: PD00794; RIBONUCLEASE.

DR PRODOM: PD000535; RnaseA; 1.

DR SMART: SMO0092; Rnase_Pc; 1.

DR PROSITE: PS00127; Rnase_PANCREATIC; 1.

KW Hydrolase; Nuclease; Endonuclease.

FT DISULFID 26 84

FT DISULFID 40 95

FT DISULFID 58 110

FT DISULFID 65 72

FT ACT_SITE 12 12

FT ACT_SITE 41 41

FT ACT_SITE 119 119

FT VARIANTS 1 1

FT SEQUENCE 124 AA: 13870 MW: 609C7E251A7BBA25 CRC64;

Query Match 22.2%; Score 128; DB 1; Length 124;

Best Local Similarity 30.6%; Pred. No. 3.7e-07;

Matches 37; Conservative 18; Mismatches 34; Indels 32; Gaps 7;

QY 4 LTFQKKHL-----TNTDVCNIIIM--STNLFHCKRKNFTYSRPEVKAICKGITA 53

DB 6 MKFOROHMDSDGHPDNTN--YCNEKMYRSMTOGRCKEVNTEFVHEPLDAVAVC---S 59

QY 54 SKNV-----LTSEFVSLDCNVTSR---CKYKLKSTNFCVTCEN--QAPVH 97

DB 60 QKNVPCKNQOTNCYOSHSSMRITDCRVYSSSKTPKNCSTYKTAOKSIIVACEGTSVPVH 119

QY 98 F 98

DB 120 F 120

RESULT 8

RNPB_CAVPO STANDARD: PRT: 128 AA.

ID RNPB_CAVPO

AC P00679;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-FEB-1994 (Rel. 28, Last annotation update)

DE Ribonuclease pancreatic B (EC 3.1.27.5) (Rnase IB).

OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavillidae; Cavia.

OX NCBI_Taxid=10141;

DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	01-NOV-1997 (Rel. 35, Last annotation update)
DE	RIBONUCLEASE pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
OS	RYNASE1 OR RNS1.
OS	Myocastor coypus (Coypu) (Nutria).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Hystriolognathi; Myocastoridae;
OC	Myocastor.
OX	NCBI_TaxId=10157;
RN	11
RP	SEQUENCE.
RC	TISSUE=Pancreas;
RC	MEDLINE=77065676; PubMed=999896;
RA	van den Berg A.; van den Hende-Timmer L.; Beintema J.J.;
RT	"Isolation, properties and primary structure of coypu and chinchilla
RT	pancreatic ribonuclease.";
RL	Biochim. Biophys. Acta 453:400-409(1976).
CC	-1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-
CC	phosphomononucleotides and 3'-phosphooligonucleotides ending in C-
CC	P or U-P with 2',3'-cyclic phosphate intermediates.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- TISSUE SPECIFICITY: PANCREAS.
CC	-1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR	PIR: A00822; IRSN.
DR	HSSP: P00656; ISRN.
DR	InterPro: IPR001427; RNaseA.
DR	Pfam: PF000074; rnasea: 1.
DR	PRINTS: PR00794; RIBONUCLEASE.
DR	ProDom: PD000535; RNaseA: 1.
DR	SMART: SM00092; RNase_Pc: 1.
DR	PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW	Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT	DISULFID 26 84 BY SIMILARITY.
FT	DISULFID 40 95 BY SIMILARITY.
FT	DISULFID 58 110 BY SIMILARITY.
FT	DISULFID 65 72 BY SIMILARITY.
FT	ACT_SITE 12 12 BY SIMILARITY.
FT	ACT_SITE 41 41 BY SIMILARITY.
FT	ACT_SITE 119 119 BY SIMILARITY.
FT	CAROHND 34 34 N-LINKED (GLCNAC...).
SEQ	SEQUENCE 128 AA; 14267 MW; 4EB924E52B445832 CRC64;
Query Match	21.4%; Score 123; DB 1; Length 128;
Best Local Similarity	29.9%; Pred. No. 1.3e-06;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;	
QY	6 FOKKHL-----INTRDVDCNIIT-STNLF--HCKKNFTYRPEPYKACIGGIASKNV 57
DB	8 FERQHDHDSGSGSTNPNCINEMKSKSNMIOGKCKPYNFTVHEPLADYQAVC---FQKNV 63
QY	58 L-----TTSEFYLSDCNVTSRP---CKYKLKSKSTNFCVTCENO--APVHF 98
DB	64 LCKNGCTNCYQSNMNMHITDCAVTSISDYPCNSYRPSGDEKSLIVACEGNPVYPVHF 120
RESULT 11	
RNP_BALAC	STANDARD; PRT; 124 AA.
AC	P00673;
DT	21-JUL-1986 (Rel. 01, Created)
DT	21-JUL-1986 (Rel. 01, Last sequence update)
DT	30-MAY-2000 (Rel. 39, Last annotation update)
DE	Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN	RNASE1 OR RNS1.
OS	Balaenoptera acutorostrata (Mink whale) (Lesser rorqual).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC	Balaenopteridae; Balaenoptera.
OX	NCBI_TaxId=9767;
RN	11
RP	SEQUENCE.

MEDLINE=7627855; PubMed=962870;

RA Emmens M., Welling G.W., Belintema J.J.;

RT "the amino acid sequence of pike-whale (lesser-torqual) pancreatic ribonuclease.";

RL Biochem. J. 157:317-323(1976).

-I CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-phosphomonocleotides and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

CC -I SUBCELLULAR LOCATION: Secreted.

CC -I TISSUE SPECIFICITY: PANCREAS.

DR PIR: A00818; NRMK.

HSSP: P00656; ISRN.

InterPro: IPR001427; RNaseA.

pfam: PF00074; rnaasea. 1.

PRINTS: PR00794; RIBONUCLEASE.

Prodrom: PD000535; RNaseA; 1.

SMART: SMO0092; RNase_Pc; 1.

DROSITE: PS00127; RNASE_PANCREATIC; 1.

KM Hydrolase; Nuclease; Endonuclease; glycoprotein.

FT DISULFID 26 84 BY SIMILARITY.

FT DISULFID 40 95 BY SIMILARITY.

FT DISULFID 58 110 BY SIMILARITY.

FT DISULFID 65 72 BY SIMILARITY.

FT ACCT_SITE 12 12 BY SIMILARITY.

FT ACCT_SITE 41 41 BY SIMILARITY.

FT ACCT_SITE 119 119 BY SIMILARITY.

FT CAROHND 76 76 N-LINKED (GLCNAC. . .); IN 30% OF THE MOLECULES.

SQ SEQUENCE 124 AA; 14125 MW; F57475459F697E20 CRC64;

Query Match 21.2%; Score 122; DB 1; Length 124;
Best Local Similarity 28.6%; Pred. No. 1.6e+06;
Matches 34; Conservative 15; Mismatches 42; Indels 28; Gaps 6;

OY 4 LTFOKKHLLTNTRDV-----CNIINSTLFF--HCKDKNTFYISRPEPYKAICKITASK 55
DB : |::|::| :: |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
6 MKFOQRHMDSGSPNNPNYCNOAMRRKMTOGRCKRPVTFEVHESLEDEWKAVC---SQK 61

OY 56 NVL-----TTSEFLSDCNTVSrp----CRKKLKSTNYFCVNCNG"-APVHF 98
DB |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
62 NWLCNKGRNRCNESNSTMHITDCROTGSKSRYPCNAIKTSQKEKHITIIVACEGNPIYPVFH 120

RESULT 12

RNP_PROGU STANDARD: PRT: 128 AA.

ID RNP_PROGU

P04059:

DT 01-NOV-1986 (Rel. 03, Created)

DT 01-NOV-1986 (Rel. 03, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).

GN RNASE1 OR RNS1.

OS Proechinus quatuor (Casiragua).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelestomii;

OC Mammalia; Euteria; Rodentia; Hystriognathii; Echimyidae; Proechimys.

OX NCBI_TaxID=10163;

XN [1]

RP SEQUENCE.

RC TISSUE=Pancreas;

RX MEDLINE=83000399; PubMed=7115727;

RA Belintema J.J., Knoll G., Martena B.;

RT "The primary structures of pancreatic ribonucleases from African porcupine and castireaga, two hysticomorph rodent species."

RL Biochim. Biophys. Acta 705:102-110(1982).

-I CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-phosphomonocleotides and 3'-phosphooligonucleotides ending in C-P or U-P with 2',3'-cyclic phosphate intermediates.

CC -I SUBCELLULAR LOCATION: Secreted.

CC -I TISSUE SPECIFICITY: PANCREAS.

CC -I SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.

DR PIR: A00821; NRKS.

```

DR HSSP; P00656; 1SRN.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84 BY SIMILARITY.
FT DISULFID 40 95 BY SIMILARITY.
FT DISULFID 58 110 BY SIMILARITY.
FT DISULFID 65 72 BY SIMILARITY.
FT ACT_SITE 12 12 BY SIMILARITY.
FT ACT_SITE 41 41 BY SIMILARITY.
FT ACT_SITE 119 119 BY SIMILARITY.
FT CARBOHYD 34 34 N-LINKED (GLCNAC...).
SQ SEQUENCE 128 AA; 14244 MW; 2DB58093A9D5C936 CRC64;

Query Match 21.0%; Score 121; DB 1; Length 128;
Best local similarity 29.9%; Pred. No. 2,2e-06;
Matches 35; Conservative 18; Mismatches 36; Indels 28; Gaps 7;

QY 6 FQKKHL-----TNRDVDCNITM-STNLF--HCKDKNTFIYSRPEPYKALCKGIITASKNV 57
   ||::||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 8 FOROHIDSGSPSTNPYCNAMKSRNMTORCKPVNPFVHPLADYAVC-----FQKNV 63

QY 58 -----LTSEFYLSDCNVTSR-----PCKYKTKKSTNFCVTCENQ--APVHF 98
   :||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
DB 64 PCKNGSGNCEYESTSNMHTDCLRTSNKSPDCLYRTSOEKSIIYACGNDPYVPVHF 120

RESULT 13
ANGI_MOUSE STANDARD; PRT; 145 AA.
ID ANGI_MOUSE STANDARD; PRT; 145 AA.
AC P21570;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Angiogenin precursor (EC 3.1.27.-).
GN ANG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91025023; Pubmed=2222458;
RA Bond M.D., Vallee B.L.;
RT "Isolation and sequencing of mouse angiogenin DNA.";
RL Biochem. Biophys. Res. Commun. 171:988-995(1990).
RN [2]
RP PARTIAL SEQUENCE.
RC TISSUE=Serum;
RX MEDLINE=93192291; Pubmed=8448182;
RA Bond M.D., Strydom D.J., Vallee B.L.;
RT "Characterization and sequencing of rabbit, pig and mouse
RT angiogenins: discernment of functionally important residues and
RT regions.";
RL Biochim. Biophys. Acta 1162:177-186(1993).
CC -1- FUNCTION: MAY FUNCTION AS A TRNA-SPECIFIC RIBONUCLEASE THAT BINDS
CC TO ACTIN ON THE SURFACE OF ENDOTHELIAL CELLS; ONCE BOUND,
CC ANGIOGENIN IS ENDOCYTOSED AND TRANSLOCATED TO THE NUCLEUS, THEREBY
CC PROMOTING THE ENDOTHELIAL INVASIVENESS NECESSARY FOR BLOOD VESSEL
CC FORMATION. ANGIOGENIN INDUCES VASCULARIZATION OF NORMAL AND
CC MALIGNANT TISSUES. ABOLISHES PROTEIN SYNTHESIS BY SPECIFICALLY
CC HYDROLYZING CELLULAR TRNAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib.ch).
CC -----
DR EMBL; U22516; AAA91366.1; -.
DR PIR; A35932; A35932.
DR HSSP; P03950; 1A4Y.
DR MCD; MGI:88022; Ang.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; rnaaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Angiogenesis;
KW protein synthesis inhibitor; Signal.
FT SIGNAL 1 24
FT CHAIN 25 145
FT MOD_RES 25 25
FT ACT_SITE 37 37 ANGIOGENIN.
FT ACT_SITE 64 64 PYROLIDONE CARBOXYLIC ACID
FT ACT_SITE 137 137 (BY SIMILARITY).
FT DISULFID 50 104 BY SIMILARITY.
FT DISULFID 63 115 BY SIMILARITY.
FT DISULFID 81 130 BY SIMILARITY.
SQ SEQUENCE 145 AA; 16228 MW; 06944260DB764938 CRC64;

Query Match 20.6%; Score 118.5; DB 1; Length 145;
Best local similarity 35.5%; Pred. No. 4,7e-06;
Matches 27; Conservative 11; Mismatches 31; Indels 7; Gaps 3;

QY 30 CKDKNTFIYSRPEPYKALC--KGIIASKNV-LTSEFYLSDCNVTS-----RCKYKTKKS 82
   ||| |||||::||::||::||::||::||::||::||::||::||::||::||::||
DB 63 CKDVNFTLHGKSNIKALCANGANGSPYRENTLRMSKSPFVTTCKHKGSGRPPCYRASAG 122

QY 83 TNTFCVTCENQAPVHF 98
   : ||| |||||
DB 123 FRHYVIACENGLPVHF 138

RESULT 14
RNP_PIG STANDARD; PRT; 124 AA.
ID RNP_PIG STANDARD; PRT; 124 AA.
AC P00671;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Ribonuclease pancreatic (EC 3.1.27.5) (RNase 1) (RNase A).
GN RNASE1 OR RNS1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=70104197; Pubmed=5460946;
RA Jackson R.L., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. II. The
RT amino acid sequence of the reduced S-aminoethylated protein.";
RL J. Biol. Chem. 245:637-653(1970).
RN [2]
RP REVISION TO 2.
RA Wierenga R.K., Huizinga J.D., Gaastera W., Wellington G.W., Beintema J.J.;
RT "Affinity chromatography of porcine pancreatic ribonuclease and
RT reinvestigation of the N-terminal amino acid sequence.";
RL FEBS Lett. 31:181-185(1973).
RN [3]
RP DISULFIDE BONDS.
RX MEDLINE=70104198; Pubmed=4904878;
RA Phelan J.J., Hirs C.H.W.;
RT "The primary structure of porcine pancreatic ribonuclease. 3. The

```

RT disulfide bonds".
RL J. Biol. Chem. 245:654-661(1970).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 3'-
CC phosphomononucleotides and 3'-phosphonucleotides ending in C-
CC P or U-P with 2',3'-cyclic phosphate intermediates.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: PANCREAS.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
DR PIR: A00816; NRPg.
DR HSSP: P00656; ISRN.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR PRINTS: PD000355; RNaseA.
DR ProDom: PD00092; RNaseA; 1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Glycoprotein.
FT DISULFID 26 84
FT DISULFID 40 95
FT DISULFID 58 110
FT DISULFID 65 72
FT ACT_SITE 12 12
FT ACT_SITE 41 41
FT ACT_SITE 119 119
FT CARBOHYD 21 21
FT CARBOHYD 34 34
FT CARBOHYD 76 76
SQ SEQUENCE 124 AA; 13804 MW; 0AC28CDE1411845 CRC64;

Query Match 20.3%; Score 117; DB 1; Length 124;
Best Local Similarity 29.9%; Pred. No. 5.7e-06;
Matches 35; Conservative 14; Mismatches 40; Indels 28; Gaps 7;

OY 6 FOKKHLTNRDVD-----CNIMSTNLF--HCKDKNTFYSRPEPKAICKGI-1 52
DB 8 FQKQHM-----DPPSSSSNSNYCNLMKSRMNRQGRCKPNTFVHESLADYQAVCSQINV 63
OY 53 ASKNVLT-----TSEFYLDSCNVTSRP---CKYKLRKSTNFCVTCENQ--APVHF 98
DB 64 NCKNGQTCNYSNSTMTHTDRCOTGSSKYPNCAYKASQEQKHITVACEGNPVPVHF 120

RESULT 15
RN14_HUMAN STANDARD; PRT; 147 AA.
AC P34096;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Ribonuclease 4 precursor (EC 3.1.27.-) (RNase 4).
GN RNASE4 OR RNS4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RX MEDLINE=95260866; PubMed=7742370;
RA Seno M., Futami J., Tsushima Y., Akutagawa K., Kosaka M., Tada H.,
RA Yamada H.,
RT "Molecular cloning and expression of human ribonuclease 4 cDNA";
RT Biochim. Biophys. Acta 1261:424-426(1995).
RL [2]
RP SEQUENCE OF 29-147 FROM N.A.
RX MEDLINE=96091174; PubMed=7501448;
RA Rosenberg H.F., Dyer K.D.;
RT "Human ribonuclease 4 (RNase 4): coding sequence, chromosomal
RT localization and identification of two distinct transcripts in human
RT somatic tissues";
RL Nucleic Acids Res. 23:4290-4295(1995).
RN [3]

RP SEQUENCE OF 29-147.
RC TISSUE=Plasma;
RX MEDLINE=94039064; PubMed=8223579;
RA Zhou H.-M., Strydom D.J.;
RT "The amino acid sequence of human ribonuclease 4, a highly conserved
RT ribonuclease that cleaves specifically on the 3' side of uridine.";
RL Eur. J. Biochem. 217:401-410(1993).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=87100997; PubMed=3467790;
RA Shapiro R., Felt J.M., Strydom D.J., Vallee B.L.;
RT "Isolation and characterization of a human colon carcinoma-secreted
RT enzyme with pancreatic ribonuclease-like activity.";
RL Biochemistry 25:7255-7264(1986).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RX MEDLINE=96096917; PubMed=9878400;
RA Terzyan S.S., Peracaula R., de Llorens R., Tsushima Y., Yamada H.,
RA Seno M., Gomis-Ruth F.X., Coll M.;
RT "The three-dimensional structure of human RNase 4, unliganded and
RT complexed with d(Up), reveals the basis for its uridine
RT selectivity.";
RL J. Mol. Biol. 285:205-214(1999).
CC -1- FUNCTION: THIS RNASE HAS MARKED SPECIFICITY TOWARDS THE 3' SIDE
CC OF URIDINE NUCLEOTIDES.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY. BL4
CC SUBFAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----

DR EMBL: D37931; BA07150.1; -;
DR EMBL: U36775; AA96750.1; -;
DR PIR: S38272; S38272.
DR PDB: 1RNE; 29-OCT-99.
DR PDB: 2RNF; 10-NOV-99.
DR MIM: 601030; -;
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; rnaasea.1.
DR PRINTS: PR00794; RIBONUCLEASE.
DR ProDom: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc.1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydroxylase; Nuclease; Endonuclease; Signal; 3D-structure.
FT SIGNAL 1 28
FT CHAIN 29 147
FT MOD_RES 29 29
FT ACT_SITE 40 40
FT ACT_SITE 68 68
FT ACT_SITE 144 144
FT ACT_SITE 53 109
FT DISULFID 67 120
FT DISULFID 85 135
FT DISULFID 92 99
FT CONFLICT 54 54
SQ SEQUENCE 147 AA; 16840 MW; 4C24FEA249F3EC2F CRC64;
N -> D (IN REF. 2).

Query Match 20.2%; Score 116.5; DB 1; Length 147;
Best Local Similarity 32.1%; Pred. No. 7.8e-06;
Matches 36; Conservative 16; Mismatches 43; Indels 17; Gaps 7;

OY 6 FOKKHL-----TNTRDVCNIM---STNLFHCKDKNTFYSRPEPKAICK--GIASKN 56
DB 36 FLRQHVPEETGSDRYCNLMQRRKMTLYHCKRFNFHEDIMNIRISICSTNIQCKNG 95
OY 57 VLTISE--FYLSDCNVT--SRP---CKYKLRKSTNFCVTCEN--QAVHVF 100

Db 96 KMNCHGVVKTVDORDTGSSRAPNCRYRAIASFRRVVIACEGNPQVPVHFDG 147

Search completed: August 9, 2002, 20:05:58
job time: 126 sec

